

SEQUENCE LISTING

04/577,304

<110> Ma, Wu-Po
Lyamichev, Victor I.
Kaiser, Michael W.
Lyamicheva, Natalie E.
Allawi, Hatim T.
Schaefer, James J.
Neri, Bruce P.

<120> Improved Enzymes for the Detection of Specific Nucleic Acid Sequences

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<170> PatentIn Ver. 2.0

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ctggacccct	ccaacaccac	ccccgagggg	gtggcccggc	gtacggggg	ggagtggacg	1200
gaggangcgg	gggagcgggc	cctcctntcc	gagaggctct	tcngaacct	nnngcagcgc	1260
cttgaggggg	aggagaggct	cctttggctt	taccaggagg	tggagaagcc	cctttcccg	1320
gtcctggccc	acatggaggc	cacgggggtg	cggctggacg	tggcctacct	ccaggccctn	1380
tccctggagg	tggcgaggga	gatccgccgc	ctcgaggagg	aggtcttccg	cctggccggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgtcttttga	cgagctnggg	1500
cttcccgcca	tcggcaagac	ggagaagacn	ggcaagcgct	ccaccagcgc	cgccgtgctg	1560
gaggccctnc	gngaggccca	ccccatcggt	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctcaaga	acacctacat	ngacccccct	ccngncctcg	tccaccccag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccn	ctggggccaga	ggatccgccc	ggccttcgtg	1800
gccgaggagg	gntgggtggt	ggtggccctg	gactatagcc	agatagagct	ccgggtcctg	1860
gccacctct	ccggggacga	gaacctgac	cgggtcttcc	aggaggggag	ggacatccac	1920
accagaccg	ccagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggggtc	ctctacggca	tgtccgcca	ccgcctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttca	ttgagcgcta	cttccagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	cgggcgctac	gtgcccga	tcaacgccc	ggtgaagagc	2220
gtgcgggagg	cggcggagcg	catggccttc	aacatgccc	tccagggcac	cgccgcccga	2280

ctcatgaagc tggccatggt gaagctcttc ccccggtnc aggaaatggg ggccaggatg 2340
ctcctncagg tccacgacga gctggtcttc gagggcccca aagagcgggc ggagngngtg 2400
gccgcttttg ccaaggaggt catggagggg gtctatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga tgggggagga ctggctctcc gccaaaggagt ag 2502

<210> 8
<211> 833
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 8
Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
50 55 60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
65 70 75 80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85 90 95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
100 105 110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
115 120 125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
130 135 140
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
145 150 155 160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
180 185 190
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
195 200 205
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
210 215 220
Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
225 230 235 240

Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
 325 330 335
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
 405 410 415
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830
 Xaa

<210> 9
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 9
 uucgcuuucu ucccuuccuu ucucgccacg uucgccggcu uccccguca agc

53

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 10
acggggaaaag ccggcgaacg tggcgagaaa 30

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 11
attagaaagg aaggaagaa agcgaa 26

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 12
acggggaaaag ccggcgaacg tggcgagaaac 30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 13
cttgacgggg aaagccggcg aacgtggcgc 30

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 14
agaaaggaag ggaagaaagc gaa 23

<210> 15

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 15
agggagaagg caactggacc gaaggcc

27

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> This 5' end has a fluorescein label.

<220>
<221> misc_feature
<222> (35)
<223> This 3' end is modified with a dideoxynucleotide.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 16
ncgaaattaa tacgcttggtg gagaaggagt tcatn

35

<210> 17
<211> 640
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 17
gggagcccag cuaugaacuc cuucuccaca agcgccuucg guccaguugc cuucucccug 60
gggcugcucc ugguguugcc ugcugccuuc ccugccccag uacccccagg agaagauucc 120
aaagauguag ccgccccaca cagacagcca cucaccucu cagaacgaau ugacaaacaa 180
auucgguaa uccucgacgg caucucagcc cugagaaagg agacauguaa caagaguaac 240
augugugaaa gcagcaaaga ggcacuggca gaaaacaacc ugaaccuucc aaagauggcu 300
gaaaaaagau gaugcuucca aucuggauuc aaugaggaga cuugccuggu gaaaaucauc 360
acuggucuuu uggaguuuga gguauaccua gaguaccucc agaacagauu ugagaguagu 420
gaggaacaag ccagagcugu ccagaugagu acaaaaagucc ugauccaguu ccugcagaaa 480
aaggcaaaga aucuagaugc aaauaccacc ccugacccaa ccacaaaugc cagccugcug 540
acgaagcugc aggcacagaa ccaguggcug caggacauga caacucaucu cauucugcgc 600

agcuuuaagg aguuccugca guccagccug agggcucuuc

640

<210> 18
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
gctatgaact ccttctccac aagcgccttc ggtccagttg ccttctccct ggg 53

<210> 19
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 19
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
1 5 10 15
Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu
20 25 30
Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp
35 40 45
Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met
50 55 60
Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser
65 70 75 80
Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg
85 90 95
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
100 105 110
Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys
115 120 125
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
130 135 140
Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys
145 150 155 160
Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg
165 170 175
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
180 185 190
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
195 200 205

Pro Leu Gly Gln Arg Ile
210

<210> 20
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 20

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
1 5 10 15
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
20 25 30
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
35 40 45
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
50 55 60
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
65 70 75 80
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
85 90 95
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
100 105 110
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
115 120 125
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
130 135 140
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
145 150 155 160
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
165 170 175
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
180 185 190
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
195 200 205
Pro Leu Gly Gln Arg Ile
210

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

acggaacgag cgtctttcat ctgtcaatc

29

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> This 5' end is labeled with
tetrachlororfluorescein.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
nttttcaact gccgtga

17

<210> 27
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> This 5' end is modified with a biotin-streptavitin
complex.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
nucacggcag uuggugcgcc ucggaacgag gcgcacg

37

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 28
tcacggcagt tggcgccct cggaacgagg cgcacg

36

<210> 29
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (30)
<223> This 3' end is modified with an amine moiety.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 29

cggaggaagc agttggtgcg cctcgttaan

30

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (1)

<223> This 5' end is labeled with fluorescein.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 30

ntcctttctca actgcttcct ccg

23

<210> 31

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (28)

<223> This 3' end is modified with a biotin moiety.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 31

aacgaggcgc acctcaaadc tccctttn

28

<210> 32

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (1)

<223> This 5' end is labeled with fluorescein.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 32

nttttcgctg tctcgct

17

<210> 33

<211> 13

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 33
acgagcgtct ttg

13

<210> 34
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> This 5' end is labeled with fluorescein.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 34
nagcgagaca gcgaaagacg ctcggt

26

<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 35
ucacggcagu uggugcggaa cgcacg

26

<210> 36
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 36
tcacggcagt tggcgcgaa cgcacg

26

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 37
cacgaattcg gggatgctgc ccctctttga gcccaa

36

<210> 38
<211> 34

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 38
gtgagatcta tcactccttg gcggagagcc agtc

34

<210> 39
<211> 2502
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 39
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttoGCCaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaaG gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccggggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggT caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggg ggccgggtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctccgccc ggcgacgacc ccattgctcct cgcctacctc 1140
ctggaccctt ccaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtggggggagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320

gtcctggccc acatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgggga gatcgccgc ctcgaggccg aggtcttcg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 tcccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccggggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggttg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacgacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaggagt ga 2502

<210> 40
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 40
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

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Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	325	330	335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	340	345	350	
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	355	360	365	
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	370	375	380	
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 41
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 41
cacgaattcc gaggcgatgc ttccgctc

28

<210> 42
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 42
tcgacgtcga ctaacccttg gcggaaagcc

30

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 43
gcatcgctc ggaattcatg gtc

23

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 44

atagccatgg tggagcggcc gctctcccgg

30

<210> 45

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 45

aagcgtcgac tcaatcctgc ttcgcctcca gcc

33

<210> 46

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 46

aatcgaattc accccacttt ttgacctga gg

32

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 47

ccgggagagc ggccgctcca c

21

<210> 48

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 48

atggaattca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60

ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120

ccggtgcaga tggctctacgg cttegcccg agcctcctca aggccttgaa ggaggacgga 180

caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240

gcctacaagg cgggccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300

[illegible]

tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc ccgggtccgc 2220
 tccgtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac 2340
 ctctctctcc aagtgcacga cgagctggtc ctggaggtgc ccgaggaccg ggccgaggag 2400
 gccaaagggc tggtcaagga ggtcatggag aacgcctacc ccctggacgt gccctcgag 2460
 gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggattga 2508

<210> 49
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 49
 actggaattc ctgccctct ttgagccaa g 31

<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 50
 aacagtcgac ctaggccttg gcggaaagcc 30

<210> 51
 <211> 2499
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 51
 atggaattcc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cgccaccac 60
 ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgagg ggagccggtc 120
 caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180
 gtgatcgtgg tgtttgacgc caaggccccc tccttcgcc accagaccta cgaggcctac 240
 aaggcggggc gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag 300
 atggtggacc ttttgggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc 360
 ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg 420
 gaccgggacc ttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac 480

ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540
 taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag 600
 aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg 660
 gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag 720
 ctatccctgg agctatcccc ggtgcacacg gacttgetcc ttcaggtgga cttcgcccg 780
 cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggtgga gttcgggaagc 840
 ctctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg 900
 cccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag 960
 cttaacgcct tggccgccgc ctgggaggga agggtttacc gggcggagga tcccttggag 1020
 gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc 1080
 ctgagggaag ggattgccct ggcaccgggc gacgaccca tgctcctcgc ctacctctg 1140
 gatccttcca acaccgcccc cgaaggggta gcccggcgt acggggggga gtggaccgag 1200
 gaggcggggg aaagggcgt gctttccgaa aggcctttac ccgccctcct ggagcggcctt 1260
 aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcggtc 1320
 ctggcccaca tggaggccac ggggggtacg ttggatgtgg cctacttaaa ggccctttcc 1380
 ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat 1440
 cctttcaacc tgaactcccc ggaccagctg gaaagggtca tctttgacga gcttgggctt 1500
 cccgccatcg gcaagacgga gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560
 gccttgccgg aggcctcatcc catcgtggac cgcctcctc agtaccggga gctttccaag 1620
 ctcaaggga cctacatcga tcccttgctt gccttggtcc accccaagac gaaccgcctc 1680
 cacaccggt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatcctaata 1740
 ctgcaaaata tccccgtgcg caccctttt ggccagcgga tccgcccggc cttcgtggcc 1800
 gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg 1860
 cacctttccg gggacgagaa cctaatacgg gtcttccagg agggccagga catccacacc 1920
 cagacggcca gctggatggt cggcgtgccc ccagaggccg tggattccct gatgcgccg 1980
 gcggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcggga 2040
 gagctggcca tcccctacga ggaggcgtg gccttcatcg agcggtatct ccagagctac 2100
 cccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg 2160
 gaaaccctct ttggccgccg gcgctacgtg cccgacttgg cttcccggtt gaagagcatc 2220
 cgggaggcag cggagcgcat ggccttcaac atgccggtcc aggggaccgc cgcggatttg 2280
 atgaaactgg ccatggtgaa gctctttccc aggcctcagg agctgggggc caggatgctt 2340

ttgcaggtgc acgacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400
caggaggcca agcggaccat ggaggaggtg tggccctga aggtgccctt ggagggtgaa 2460
gtgggcatcg gggaggactg gctttccgcc aaggcctag 2499

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 52
cgatctcctc ggccacctcc 20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 53
ggcgtgccc tggacgggca 20

<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 54
ccagctcggt gtggacctga 20

<210> 55
<211> 2505
<212> DNA
<213> Thermus aquaticus

<220>
<221> CDS
<222> (1)..(2499)

<400> 55
atg aat tgc ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144

ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg	1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	
450 455 460	
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc	1440
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	
465 470 475 480	
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt	1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	
485 490 495	
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag	1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys	
500 505 510	
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc	1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro	
515 520 525	
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc	1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser	

530	535	540	
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc 1680			
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg			
545 550 555 560			
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt 1728			
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser			
565 570 575			
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg 1776			
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly			
580 585 590			
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg 1824			
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val			
595 600 605			
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc 1872			
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser			
610 615 620			
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac 1920			
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His			
625 630 635 640			
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac 1968			
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp			
645 650 655			
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac 2016			
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr			
660 665 670			
ggc atg tgc gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag 2064			
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu			
675 680 685			
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg 2112			
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val			
690 695 700			
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac 2160			
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr			
705 710 715 720			
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc 2208			
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala			
725 730 735			
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg 2256			
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met			
740 745 750			
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag 2304			
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys			
755 760 765			
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc 2352			
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val			
770 775 780			

cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg 2400
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg 2448
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag 2496
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

gag tgatag 2505
 Glu

<210> 56
 <211> 833
 <212> PRT
 <213> Thermus aquaticus

<400> 56
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Glu

<210> 57
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 57

caggaggagc tcgttggtgga cctgga

26

<210> 58

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 58

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu

255

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 59

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 59

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccagag acttccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgaggtccc cggctacgag 360
gcgacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960
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gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctgctgccc gggacgacct catgctcttc 1140
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gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
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caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500
gagcttaggc ttcccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920

ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccca aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 63
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 63
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 64
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 64

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgaggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcctc acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagtccggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtgggagg agcttaaagc cctggccgcc tgcagggacg gccgggtgca ccgggcagca 1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140
gcctacctcc tggaccttc caacaccacc cccgaggggg tggcgcgcg ctacgggggg 1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggg ggaaaagccc 1320
ctctcccggg tcctggccca catggaggcc accggggtac ggcgggacgt ggctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500
gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740

tccgacccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgctctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttggcgctc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaggt gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccaccc caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt ccacaacgag ctctcctgg aggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 65
<211> 842
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 65
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 70

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcctg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc 960
atgtggggcg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gacccttg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
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gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740

tccgacccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgccgg 1800
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cgcgctctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttccggcgcc ccccgaggc cgtggacccc 1980
ctgatgcgcc gggcgcccaa gacggtgaac ttccggcgcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tcccaaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
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gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt ccacaacgag ctctctctgg agggccccca agcgcggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggttttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 71
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 71
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcac 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggagggt	ggacttcgcgc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagagggt	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
aaagccctca	gggacctgaa	ggaggcgcgg	gggcttctcg	ccaaagacct	gagcgttctg	1080
gccctgaggg	aaggccttgg	cctcccgccc	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcccggc	gctacggcgg	ggagtggacg	1200
gaggaggcgg	gggagcgggc	cgccctttcc	gagaggctct	tgcccaacct	gtggggggagg	1260
cttgaggggg	aggagagggt	cctttggctt	taccgggagg	tggagaggcc	cctttccgct	1320
gtcctggccc	atatggaggc	cacgggggtg	cgcctggacg	tggcctatct	cagggccttg	1380
tccctggagg	tggccgagga	gatcgcccg	ctcgaggccg	aggtcttccg	cctggccggc	1440
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aagctgaaga	gcacctacat	tgacccttg	ccggacctca	tccaccccag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgcgg	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	cagggtgctg	1860
gcccacctct	ccggcgacga	gaacctgatc	cgggtcttcc	aggagggggc	ggacatccac	1920
acggagaccg	ccagctggat	gttcggcgtc	ccccgggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcgggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	ccgccgctac	gtgccagacc	tagaggcccg	ggtgaagagc	2220
gtgcgggagg	cggccgagcg	catggccttc	aacatgccc	tccagggcac	cgccgccgac	2280
ctcatgaagc	tggctatgg	gaagctcttc	cccaggctgg	aggaaatggg	ggccaggatg	2340
ctccttcagg	tccacaacga	gctggctctc	gaggcccaa	aagagagggc	ggaggccgtg	2400
gcccggctgg	ccaaggagg	catggagggg	gtgtatcccc	tggccgtgcc	cctggagggtg	2460
gaggtgggga	taggggagga	ctggctctcc	gccaaaggag	accaccacca	ccaccac	2517

<210> 72

<211> 842
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 72

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
		180						185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
			245						250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
		260						265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 73
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 73
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile

60

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 74
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 74
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cggggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 75

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 76
 <211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 76

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
 ctcataaagg agctggtgga cctcctggggg ttaccgccg tgcaggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420

gccgccgacc tcatgaagct ggctatgggtg aagctcttcc ccaggctgga ggaaatgggg 2340
 gccaggatgc tccttcaggt ccacaacgag ctggctcctcg aggccccaaa agagagggg 2400
 gagggcgtgg cccggctggc caaggaggtc atggagggggg tgtatcccct ggccgtgccc 2460
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520
 caccac 2526

<210> 77
 <211> 842
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 77
 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu
 405 410 415
 Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp
 420 425 430
 Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser
 450 455 460
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp
 595 600 605
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg
 625 630 635 640
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala
 785 790 795 800
 Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Glu His His His His His His
 835 840

<210> 78

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 78

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcbc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggcct agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcgcg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
gatctttctg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccattgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgcgc ccacccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
cttcccgcct tggggaagac gcaaaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggcccgc 1680
ctccacacc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860

gccacacctt cggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cggcgggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaggagc accaccacca ccaccac 2517

<210> 79
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 79
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Glu His His His His His
835

<210> 80
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 80
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggcctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg cttcttgaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260
cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc ctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcttgacg tggcctatct cagggccttg 1380
tccttgagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500

cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
 gaggcctcc gcgaggcca ccccatcggtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcgtg 1800
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
 gccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggtctctc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccagcc tcaacgcccg ggtgaagagc 2220
 gtcaggaggc ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcagc 2340
 ctctccagg tccacaacga gctctctctg gaggccccc aagcgcgggc cgaggaggtg 2400
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccagggtc accaccacca ccaccac 2517

<210> 81
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 81
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	435	440	445
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	450	455	460
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	465	470	475
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	485	490	495
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys	500	505	510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro	515	520	525
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser	530	535	540
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg	545	550	555
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser	565	570	575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly	580	585	590
Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val	595	600	605
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser	610	615	620
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His	625	630	635
Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp	645	650	655
Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr	660	665	670
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu	675	680	685
Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	690	695	700
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr	705	710	715
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala	725	730	735
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	740	745	750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	755	760	765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Gly Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 82
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 82
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gcccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
 gcggggctaa aggacctcaa ggaggtccgg ggctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140

ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcga tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcggt gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800
gcgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
ctcatgaagc tggctatggt gaagctcttc ccaggttgagg aggaaatggg ggccaggatg 2340
ctccttcagg tcacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 83

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 83

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	

Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 84
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 84
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgagg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtcttgccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
 tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
 cttcccgctt tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
 aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
 aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggccc ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 85
 <211> 839
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 85

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 86

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 86

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgccg gaggacttcc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacctc 420

accgcccagaca	aagacaccttta	ccagctcctt	tccgaccgcga	tccacgtcct	ccacccccgag	480
gggtacctca	tcacccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	ggggccctgac	cgggggacgag	tccgacaacc	ttcccgggggt	caaggggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggagggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggaggga	ggccccctgg	900
ccccgcgcgg	aaggggcctt	cgtggggctt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatctttctg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
aaagccctca	gggacctgaa	ggaggcgcg	gggcttctcg	caaagacct	gagcgttctg	1080
gccttgagg	aaggccttgg	cctcccgccc	ggcgacgacc	ccatgtcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttcccgcc	tggggaagac	gcaaaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccct	ccaagcctcg	tccacccgag	gacggggcgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcatc	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	cagggtgctg	1860
gccacctct	ccggcgacga	gaacctgac	cgggtcttcc	aggagggggc	ggacatccac	1920
acggagaccg	ccagctggat	gttcggcgtc	ccccgggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagacct	tcttcggccg	ccgcgcgtac	gtgccagacc	tagaggcccc	ggtgaagagc	2220
gtgcggggagg	cggccgagcg	catggccttc	aacatgccc	tccagggcac	cqccqccqac	2280

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tccacaacga gctggtcctc gagggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 87
<211> 839
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 87
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 88

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 88

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccgcc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccattgctcct cgcctacctc 1140
ctggacctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc cgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcga tcggcaagac ggagaagacc ggcaagcgct ccaccagcg cgccgtcctg 1560
gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccttgg ccggacctca tccacccag gacgggccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa ctctcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggtctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gagggcccaa aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 89
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 89
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 90
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 90
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgccc tcgagggtccc cggtacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc 960
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgccccg gggacgaccc catgctcctc 1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg 1200
gagtggacgg aggacgccc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagggt ggaaaagccc 1320
ctctccccgg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggacctctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc 1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500
gagcttaggc ttcccgctt ggggaagacg caaaagacag gcaagcgtc caccagcgcc 1560

gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
 gagtcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680
 acgggccgccc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
 tccgacccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg 1800
 gccttcacg ccgaggagggt gtggctattg gtggccctgg actatagcca gatagagctc 1860
 aggggtgctgg cccacctctc cggcgacgag aacctgatcc gggtcttcca ggaggggagg 1920
 gacatccaca cggagaccgc cagctggatg ttcggcgctcc cccgggaggc cgtggacccc 1980
 ctgatgcgcc gggcgcccaa gaccatcaac ttcgggggtcc tctacggcat gtcggccac 2040
 cgcctctccc aggagctagc catcccttac gaggaggccc aggccttcat tgagcgctac 2100
 tttcagagct tccccaaagt gcgggcctgg attgagaaga ccctggagga gggcaggagg 2160
 cgggggtacg tggagaccct cttcgccgc cgcgctacg tgccagacct agaggcccgg 2220
 gtgaagagcg tgcgggaggc ggccgagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct ggctatggtg aagctcttcc ccaggctgga ggaaatgggg 2340
 gccaggatgc tccttcaggt ccacaacgag ctggtcctcg agggccaaa agagagggcg 2400
 gaggccgtgg cccggctggc caaggaggtc atggaggggg tgtatccct ggccgtgccc 2460
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520
 caccac 2526

<210> 91
 <211> 842
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 91
 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp
 595 600 605
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg
 625 630 635 640
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala
785 790 795 800

Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Glu His His His His His His
835 840

<210> 92
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 92
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccc acccccgagg acttccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360
gcggaacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac 480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtcca ccgggcccc 1020
gagccttata aagccctcag ggacctgaag gaggcggggg ggcttctcgc caaagacctg 1080
agcgttctgg ccctgaggga aggccttggc ctcccgcccc gcgacgacct catgctcctc 1140

gcctacctcc tggacccttc gaacaccacc cccgagggggg tggcccggcg ctacggcggg 1200
gagtggacgg aggaggcggg ggagcgggcc gccctttccg agaggctctt cgccaacctg 1260
tgggggagggc ttgaggggga ggagaggctc ctttggcttt accgggaggt ggagaggccc 1320
ctttccgctg tcttgccca tatggaggcc acgggggtgc gcctggacgt ggcctatctc 1380
agggccttgt ccctggaggt ggccgaggag atcgcccgcc tggaggccga ggtcttccgc 1440
ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt cctctttgac 1500
gagctagggc ttcccgccat cggcaagacg gagaagaccg gcaagcgctc caccagcgcc 1560
gccgtcctgg agggcctccg cgaggccac cccatcgagg agaagatcct gcagtaccgg 1620
gagctcacca agctgaagag cacctacatt gacccttgc cggacctcat ccaccccagg 1680
acgggcccgc tccacaccg cttcaaccag acggccacgg ccacgggcag gctaagtagc 1740
tccgatccca acctccagaa catccccgtc cgcacccgc ttgggcagag gatccgccc 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc 1980
ctgatgcgcc gggcgccaa gacgggtgaac ttcggcgctc tctacggcat gtccgccc 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcagtc tctccaggt ccacaacgag ctctcctgg agggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 93

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 93

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	

Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65					70					75				80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
	145					150					155				160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
	225					230					235				240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
	305					310					315				320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala
			340					345					350		

Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu
 405 410 415
 Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp
 420 425 430
 Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser
 450 455 460
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 94

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 94

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcttacggg 240
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

<210> 95
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 95

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Gly

<210> 96
 <211> 2499
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 96
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacggg 240
 ggggtacaagg cggggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300

gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcccttcagg tccacgacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag 2499

<210> 97
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 97
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Glu

<210> 98
 <211> 2499
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 98

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgcgc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
gatctttctg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccattgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccaggggg gtggcccggc gctacggcgg ggagtgagc 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260
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gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
tccttgagg tggccgagga gatcgcgcgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc cggggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcga tcggcaagac ggagaagacc ggcaagcgtc ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccttgg ccggacctca tccacccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740

aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcgtg 1800
 gccgagggcg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
 gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc 2220
 gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcacg 2340
 ctctccagg tccacgacga gctcctctg gagggcccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggt 2499

<210> 99
 <211> 833
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 99
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265						270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
			325						330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
			405					410						415	
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
			420					425					430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
	450					455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly

<210> 100
<211> 2499
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 100
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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380

Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 102
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 102
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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc ccccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgccc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcgagg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020

aaagccctca gggacctgaa ggaggcgcg gggtctctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
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tccctggagc ttgcggagga gatccgccc ctcgaggagg aggtcttccg cttggcgggc 1440
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gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
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cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagacc tcttcggccg ccgcccgtac gtgccagacc tagaggccc ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgcgcggac 2280
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 103
<211> 839
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 103
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly His Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 104

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 104

gaggaggcgg ggcaccgggc cgccctt

27

<210> 105

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 105

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccgggc ccccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcg accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggccttcc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctcc atcggaacct gtgggggagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
cttccgcct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
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acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcgccca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160

210	215	220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240		
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255		
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270		
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285		
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300		
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320		
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 335		
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350		
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365		
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380		
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400		
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu His Arg Asn 405 410 415		
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430		
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445		
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu 450 455 460		
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly 465 470 475 480		
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495		
Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys 500 505 510		
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525		
Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn 530 535 540		

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 107

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 107

ctttccgaga ggctccatcg gaacctgtgg gggagg

36

<210> 108

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 108

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag cgggggggag 120
cgggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggcctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc cttttccgct 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380

tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
 cttcccgct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
 aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacggggccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
 aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 109

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 109

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

<210> 112
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 112

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
	195						200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
		260						265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 113
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 113
 agggcccttt cccgggtcct ggcccat

27

<210> 114
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 114

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccg ggggacgacc ccatgctcct cgcctacctc 1140
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gaggacgcgc ccacccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
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gtcctggccc atatggaggc cacgggggtg cgccgggacg tggcctatct cagggccttg 1380
tccttgaggg tggccgagga gatcgccgcg ctcgaggccg aggtcttcg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860

gccacacctt cggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cggcgggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 tcccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgcgcctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgcccac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaggagc accaccacca ccaccac 2517

<210> 115
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 115
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	500	505	510
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780
His	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	785	790	795
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	805	810	815
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	820	825	830

Glu His His His His His His
835

<210> 116
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 116
acgggggtgc gccgggacgt ggcctat 27

<210> 117
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 117
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttegccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccggggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc 1140

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
370						375					380					
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
385					390					395					400	
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	
				405					410					415		
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	
			420					425					430			
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	
450						455					460					
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505						510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515					520					525				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
530						535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
545					550					555					560	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565				570						575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
		610				615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625					630					635					640	
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
				645					650					655		
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
			660					665					670			
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680					685				
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
		690				695					700					

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 119

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 119

gtggcctatc tccaggcctt gtcctg

27

<210> 120

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 120

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccag	480
gggtacctca	tcaccccggc	ctggctttgg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcg	accgacctgc	ccctggagg	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagg	ggccccctgg	900
ccccgcggg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggagggtccg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccg	1320
gtcctggccc	atatggaggc	cacgggggtg	cgcctggacg	tggcctatct	cagggccttg	1380
tccctggagc	ttgccgagga	gatcgcccg	ctcgaggccg	aggtcttccg	cctggccggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tcctctttga	cgagctaggg	1500
cttcccgcca	tcggcaagac	ggagaagacc	ggcaagcgct	ccaccagcgc	cgccgtcctg	1560
gaggccctcc	gcgaggccca	ccccatcg	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctgaaga	gcacctacat	tgaccccttg	ccggacctca	tccaccccag	gacggggcgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgccg	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	cagggtgctg	1860
gccacctct	ccggcgacga	gaacctgac	cgggtcttcc	aggagggggc	ggacatccac	1920
acggagaccg	ccagctggat	gttcggcg	ccccgggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	ccgcgcgtac	gtgccagacc	tagaggcccg	ggtgaagagc	2220
gtgcggggagg	cggccgagcg	catggccttc	aacatgcccc	tccagggcac	cgcgcgcgac	2280

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tccacaacga gctggctcctc gaggcccca aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 121

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 121

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 122

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 122

ttgtccctgg agcttgccga ggagatc

<210> 123
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 123
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc tccccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc cctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
 gcggggctaa aggacctcaa ggaggtccgg ggctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccattgctcct cgctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
 gaggacgcgc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
 gtctggcccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatccgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

0047304 052400

gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggacce cctgatgcgc 1980
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 124
<211> 839
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 124
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Glu His His His His His His
 835

<210> 125
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 125
 gccgaggaga tccgccgcct cgaggcc 27

<210> 126
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 126
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cggggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
 gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcgccgc gctacggggg ggagtggacg 1200
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
 gtccctggccc atatggaggc cacgggggtg cgccctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggagg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggtcttc gaggcccaa aagagagggc ggaggccgtg 2400
 gccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 127
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 127

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

00430 402450

305	310	315	320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala		
	325	330	335
Ala Asp Pro Leu	Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu		
	340	345	350
Leu Ala Lys Asp	Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu		
	355	360	365
Val Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser		
	370	375	380
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr		
	385	390	400
Glu Asp Ala Ala	His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn		
	405	410	415
Leu Leu Lys Arg	Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His		
	420	425	430
Glu Val Glu Lys	Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr		
	435	440	445
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val		
	450	455	460
Ala Glu Glu Ile	Ala Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly		
	465	470	475
His Pro Phe Asn	Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe		
	485	490	495
Asp Glu Leu Gly	Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys		
	500	505	510
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro		
	515	520	525
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser		
	530	535	540
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg		
	545	550	555
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser		
	565	570	575
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly		
	580	585	590
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val		
	595	600	605
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser		
	610	615	620
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His		
	625	630	635
			640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 128

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 128

gccccgctcg aggaggaggt cttccgc

27

<210> 129

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 129

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccccccagag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgcctcccg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caagggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgcccg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttctgg ccctggccgc cgcaggggc ggcgcgtgc accgggcagc agacccttg 1020
 gcggggctaa aggacctcaa ggaggctccg ggcctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgcc ggggacgacc ccatgctcct cgcctacctc 1140
 ctggacctt cgaacaccac cccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
 gtctggccc atatggagge cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaact cggggaccag ctggaaaggg tcctctttga cgagctaagg 1500
 cttcccgcga tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560
 gaggcctcc gcgaggcca cccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccttg ccggacctca tccaccccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctcaga acatccccgt ccgcacccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggcg ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980
 cgggcgcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gagggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 130

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 130

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
	115						120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150				155					160	
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

<210> 131
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 131
tttgacgagc taaggcttcc cgccatc

27

<210> 132
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 132
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcgagg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggac 960
gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccg ggggacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcgcggc gctacggggg ggagtggacg 1200

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 134
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 134
atcgccaaga cgcaaaagac cggcaag

27

<210> 135
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 135
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag 480

ggggtacctca tcaccccgcc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600
 ggggagaaga cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgccc accgacctgc cctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga gggccctcgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
 gcggggctaa aggacctcaa ggaggtccgg ggccctcctc ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcgccgc gctacggggg ggagtggacg 1200
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320
 gtccctggcc atatggaggc cacgggggtg cgccctggac tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgtc ccaccagcgc cgccgtcctg 1560
 gaggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagcaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccacccag gacgggccgc 1680
 ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctcaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 tcccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340

ctccttcagg tccacaacga gctggtcctc gaggcccca aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 136
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 136
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu

245										250										255																									
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala																														
			260						265						270																														
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu																														
			275				280							285																															
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu																														
			290				295				300																																		
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala																														
			305			310				315					320																														
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala																														
				325					330					335																															
Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu																														
			340					345					350																																
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu																														
			355				360						365																																
Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser																														
			370			375					380																																		
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr																														
			385			390				395				400																															
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn																														
				405					410					415																															
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His																														
			420					425					430																																
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr																														
			435				440					445																																	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val																														
			450			455					460																																		
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly																														
			465			470				475				480																															
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe																														
				485					490					495																															
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys																														
			500					505					510																																
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro																														
			515				520					525																																	
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser																														
			530			535						540																																	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg																														
			545			550				555				560																															
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser																														
				565					570					575																															

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 137

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 137

aagatcctgc agcaccggga gctcacc

27

<210> 138
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 138
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgcctcctc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccattgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcgcc gctacggggg ggagtggacg 1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggg cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
tccttgagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

gagggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga acacctacat tgacccttg cgggacctca tccaccccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcacccccg cttgggcaga ggatccgccc ggcccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgcgcctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgcgcgcgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctccctcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 139

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 139

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110

Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	

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 gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
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 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
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 aagctgaaga gcacctacgt ggacccttg ccggacctca tccaccag gacgggccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
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 gtggagacct tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
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 ctccctcagg tccacaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400
 gccgggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 142
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 142

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 143

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 143

aagagcacct acgtggaccc cttgccg

27

<210> 144

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 144

atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacggg 240
gggtacaagg cgggccggggc ccccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
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cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
gcgggggctaa aggacctcaa ggaggctcgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140
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gaggacgccg ccacccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
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tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440
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cttcccgcga tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
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aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgaggagg cagtggaccc cctgatgcgc 1980
 cgggaggcca agaccatcaa ctctgggggc ctctacggca tgcgggcca ccgcctctcc 2040
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 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
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 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 145

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 145

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
						135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 146
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 146
attgacccct tgccgagcct cgtccacccc aggacgggc

39

<210> 147
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 147
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cggggcgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgctcagagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
gggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcgagg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accggggccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgagg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgctacctc 1140
ctggaccctt cgaacaccac ccccaggggg gtggcccgcc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgcccg ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggacc cctgatgcgc 1980
cgggcggcca agaccatcaa ctccggggtc ctctacggca tgtcggcca ccgcctctcc 2040
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ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagacc tcttcggccg ccgcgcctac gtgccagacc tagaggccc ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgcccac 2280
ctcatgaagc tggtatggg gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tcacaaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaggagc accaccacca ccaccac 2517

<210> 148

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 148

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5				10						15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20					25					30			
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
	35					40					45				

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	420	425	430	
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 149

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 149

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cggggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgccg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccattgctct cgctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttgggagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtcctggccc atatggaggc cacgggggtg cgcttgagcg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgt ccaccagcg cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccacccag gacgggccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggccc ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 150
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 150

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 151

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 151

ttcgccaacc tgcttgggag gcttgagggg gag

33

<210> 152

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 152

atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60

acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgccccgagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 153

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 153

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105						110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
		130				135						140			
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170						175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 154
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 154
 ctcttcgccca acctgtggaa gaggcttgag ggg

33

<210> 155
 <211> 835
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 155
 Met Glu Phe Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
 20 25 30
 Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
 35 40 45
 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg

004250 402400

210	215	220
Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp 225 230 235 240		
Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu 245 250 255		
Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly 260 265 270		
Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu 275 280 285		
Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro 290 295 300		
Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro 305 310 315 320		
Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Glu Gly Arg Val 325 330 335		
His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala 340 345 350		
Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly 355 360 365		
Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu 370 375 380		
Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly 385 390 395 400		
Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu 405 410 415		
Phe Gln Asn Leu Phe Pro Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr 420 425 430		
Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala 435 440 445		
Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu 450 455 460		
Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala 465 470 475 480		
Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu 485 490 495		
Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Glu Lys Thr Gly 500 505 510		
Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His 515 520 525		
Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys 530 535 540		

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
770 775 780

Val His Asp Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu
785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala
820 825 830

Lys Gln Asp
835

<210> 156

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 156

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctggggg tttaccgcgc tcgaggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac 480
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtggggg gacccctccg acaacctccc cgggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
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gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgacct catgctcctc 1140
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 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
 gacatcgcca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcgccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt ccacaacgag ctctccttgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 157

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 157

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85					90						95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120						125		

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile Ala Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 158

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 158

gcttgcggtc tgggtggcga tgccttccc etc

33

<210> 159

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 159

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg ttaccgccg tccaggtccc cggctacgag 360
gcgagcgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctaccaa ctctgtccg accgctcgc cgtcctccac 480
cccgagggcc acctcatcac ccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttccg ggagagggtg 840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960

<400> 160

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val

004350 404 004400

325										330					335				
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val				
			340					345					350						
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly				
		355					360					365							
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu				
	370					375					380								
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly				
	385				390					395					400				
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu				
				405					410					415					
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp				
			420					425					430						
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met				
		435					440					445							
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser				
		450				455					460								
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg				
	465				470						475				480				
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg				
				485				490						495					
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys				
			500					505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535					540								
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
	545				550						555				560				
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
				565					570					575					
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
			580					585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
		610				615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
	625				630						635				640				
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
				645					650					655					

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Ala Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 161
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 161
catgttgaag gccatggcct ccgcggcctc cct

33

<210> 162
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 162
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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctggggg tttaccgccg tcgaggtccc cggctacgag 360
gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac 480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtggggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
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acgggcccgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
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gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgctcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc 1980

ctgatgcgcc gggcgggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tcccgaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220
gtgaagagcg tcaggaggcg cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctccttgg agggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 163

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 163

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85						90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
	145				150					155				160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
			165						170					175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 164
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 164
caggaggagc tcgttggcga cctggaggag

30

<210> 165
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 165
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgaggtccc cggctacgag 360
gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc agggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtggggcg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020
gacccttg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg 1200

gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgaccca	acctgcagaa	catccccgtc	cgcaccccc	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgctctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccat	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccg	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgctccg	ggagatgggg	2340
gcccgcatgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggtca	ccaccaccac	2520
caccac						2526

<210> 166

<212> PRT

<220>

<400> 166

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100				105						110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 167
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 167
ggagcgcttg cctgtcttct tcgtcttctt caaggcgga ggcct 45

<210> 168
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 168
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag 480
 ggggtacctca tcacccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgctc accgacctgc ccctggagggt ggacttcgcc 780
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 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 cccccgccgg aaggggcctt cgtgggcctt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgagg gggccttctc ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
 gtcttgccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccttctg ccggacctca tccaccccag gacgggcccgc 1680
 ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgac cggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggacct cctgatgcgc 1980
 cgggcgggca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttcccaagg tcggggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 169
<211> 839
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 169
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 170

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 170

gaggaccagc tcgttggcga cctgaaggag cat

33

<210> 171
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 171

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atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
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cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

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gaggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccacccag gacgggcccgc 1680
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 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
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<210> 172

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 172

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85						90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105						110	

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile Ala
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

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gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 175
<211> 839
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 175

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

305		310		315		320									
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325					330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345						350	
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
				405					410					415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
			420					425					430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
	450					455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
	530					535					540				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Ala	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His
625					630					635					640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 176

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 176

cagaacatcc ccgtcgccac cccgcttggg cag

33

<210> 177

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 177

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60

acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccaggggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tgcccaacga gctggtcctc gagggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 178

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 178

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170						175

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 179
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 179
gggcttcccg ccatcaagaa gacggagaag acc

33

<210> 180
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 180
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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacgag 240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccatgtcctc cgctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtccctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgcccg ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacggggcgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa ctctgggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 181

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 181

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5				10						15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 182
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 182
ctagggcttc ccgcatcaa gaagacgcaa aagaccggc 39

<210> 183
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 183
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cgagacggag gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacccctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

ctccttcagg tcgccaacga gctgggtctc gaggcccca aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 184
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 184
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Glu Thr Glu Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu

245							250							255			
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala		
			260				265						270				
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu		
		275						280						285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu		
		290						295						300			
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala		
		305						310						315			
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala		
			325						330						335		
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu		
			340						345						350		
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu		
		355						360						365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser		
		370						375						380			
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr		
		385						390						395			
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn		
			405						410						415		
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg		
			420						425						430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr		
		435						440						445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val		
		450						455						460			
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly		
		465						470						475			
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe		
			485						490						495		
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys		
			500						505						510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro		
			515						520						525		
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser		
		530						535						540			
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg		
		545						550						555			
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser		
			565						570						575		

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 185

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 185

ccggggaaag tcctcctccg tctcggcccg gcccgccctt

<210> 186
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 186
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
 ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccattgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtcttgcccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgcg ctcgaggcgg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacggggccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggcg ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggacc cctgatgcgc 1980
cgggcgccca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tcgccaacga gctggtcttc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 187

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 187

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

004250 4004 03400

Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
450						455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
530						535					540				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His
625					630					635					640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 188
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 188
cgggacctcg aggcgcgtga accccaggag gtccac 36

<210> 189
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 189
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcttacggg 240
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
gggggagaaga cggcgaggaa gcttctggag gaggggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccttgagggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggcctt agggcctttc tggagagggt tgagtttggc 840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga gggcccttg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttcttg ccctggccgc cgccaggggc ggcgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtccctggccc atatggaggg cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcggt gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttgg ccggacctca tccacccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcctc 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc cccggggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcttg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctccctcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400
 gccgggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 190
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 190

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

305		310		315		320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg	Gly Gly Arg Val His Arg Ala				
	325		330		335	
Pro Glu Pro Tyr	Lys Ala Leu Arg Asp	Leu Lys Glu Ala Arg Gly Leu				
	340		345		350	
Leu Ala Lys Asp	Leu Ser Val Leu Ala Leu Arg	Glu Gly Leu Gly Leu				
	355		360		365	
Pro Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr	Leu Leu Asp Pro Ser				
	370		375		380	
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr					
	385		390		395	400
Glu Glu Ala Gly	Glu Arg Ala Ala Leu Ser	Glu Arg Leu Phe Ala Asn				
	405		410		415	
Leu Leu Lys Arg	Leu Glu Gly Glu Glu Arg Leu Leu Trp	Leu Tyr Arg				
	420		425		430	
Glu Val Glu Arg	Pro Leu Ser Ala Val Leu Ala His	Met Glu Ala Thr				
	435		440		445	
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val					
	450		455		460	
Ala Glu Glu Ile	Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly					
	465		470		475	480
His Pro Phe Asn	Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe					
	485		490		495	
Asp Glu Leu Arg	Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys					
	500		505		510	
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro					
	515		520		525	
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser					
	530		535		540	
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg					
	545		550		555	560
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser					
	565		570		575	
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly					
	580		585		590	
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val					
	595		600		605	
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser					
	610		615		620	
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His					
	625		630		635	640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 191

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 191

ctcctccacg agttcggc

18

<210> 192

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 192

accggtcttc ttcgtcttct tcaacttggg aagcctgagc tcgtcaaa

48

<210> 193
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 193
aagacgaaga agaccggtaa gcgctccacc agc

33

<210> 194
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 194
gtcgactcta gatcagtggt ggtgggtggtg gtgcttggcc gcccggcgca tc

52

<210> 195
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<221> modified base

<222> (19)..(42)

<223> The bases in these positions within this primer
are 91% of the base shown and 3% each of the other
3 nucleotides.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 195
ggagcgctta ccggtctttt gcgtcttctt gatcttggga agccttagct cgtcaaagag 60

<210> 196
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 196
ctcctccacg agttcggc

18

<210> 197
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<221> modified_base
 <222> (19)..(42)
 <223> The bases at these positions within this primer
 are 91% of the base shown and 3% each of the other
 3 nucleotides.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 197
 caaaagaccg gtaagcgctc caccagcgcc gccgtcctgg aggccctccg cgaggccac 60

<210> 198
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 198
 gtcgactcta gatcagtggg ggtggtggtg gtgcttggcc gcccggcgca tc 52

<210> 199
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 199
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgcctcctc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccagctcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc cctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggcccccctgg	900
ccccgcgcgg	aaggggcctt	cgtgggcctt	gtgctttccc	gcaaggagcc	catgtggggcc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
aaagccctca	gggacctgaa	ggaggcgcg	gggcttctcg	ccaaagacct	gagcgttctg	1080
gccctgaggg	aaggccttgg	cctccgcgcc	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcccggc	gctacggcgg	ggagtggacg	1200
gaggaggcgg	gggagcgggc	cgccctttcc	gagaggctct	tcgccaacct	gcttaagagg	1260
cttgaggggg	aggagaggct	cctttggctt	taccgggagg	tggagaggcc	cctttccgct	1320
gtcctggccc	atatggaggc	cacgggggtg	cgcttgga	tggcctatct	cagggccttg	1380
tccctggagg	tggccgagga	gatcgccgc	ctcgaggccg	aggtcttccg	cctggccggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaagg	tcctctttga	cgagctaagg	1500
cttccaaga	tcaacaagac	gaagaagacc	ggtaagcgct	ccaccagcgc	cgccgtcctg	1560
gaggccctcc	gcgaggccca	ccccatcgtg	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctgaaga	gcacctacat	tgacccttgg	ccggacctca	tccaccccag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgcgg	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	caggggtgctg	1860
gcccacctct	ccggcgacga	gaacctgatc	cgggctcttc	aggagggggc	ggacatccac	1920
acgggagacc	ccagctggat	gttcggcgtc	ccccgggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	ccgccgctac	gtgccagacc	tagaggcccg	ggtgaagagc	2220
gtgcgggagg	cggccgagcg	catggccttc	aacatgccc	tccagggcac	cgccgccgac	2280
ctcatgaagc	tggctatgg	gaagctcttc	cccaggctgg	aggaaatggg	ggccaggatg	2340
ctccttcagg	tcgccaacga	gctggctctc	gaggcccca	aagagagggc	ggaggccgtg	2400
gcccggctgg	ccaaggagg	catggagggg	gtgtatcccc	tggccgtgcc	cctggagggtg	2460
gaggtgggga	taggggagga	ctggctctcc	gccaaaggag	accaccacca	ccaccac	2517

```
<210> 200
<211> 839
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Synthetic

<400> 200

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 201

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 201

atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacggg 240
 ggggtacaagg cgggcccgggc cccacgccc gaggaacttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tcgccaacga gctggtcctc gaggcccca aagagagggc ggaggccgtg 2400
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 202
<211> 839
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 202
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Ile Pro Lys Ile Lys Lys Thr His Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 203
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 203
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtgctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacacgcc gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cttttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgt ccagcagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacctctg ccggacctca tccacccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgaggag cctgggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgccccgagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 204

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 204

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105						110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135						140			
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170						175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

<210> 205
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 205
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccgcc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc tccccggggc caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatcccg gagaagatcc tggccacat ggacgatctg 720
 aagctctcct gggacctggc caagtgcg cccgacctgc ccctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
 gtccctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccaccagcgc cgccctcctg 1560

Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Leu	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 207
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 207
gtcggagggg tccccacga g 21

<210> 208
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 208
tgtggaattg tgagcgg 17

<210> 209
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (28)..(59)
<223> The bases in these positions within this primer
are 91% of the base shown and 3% each of the other
3 nucleotides.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 209
ctcgtggggg acccctccga caacctcccc ggggtcaagg gcatcgggga gaagaccgcc 60
ctcaagcttc tcaag 75

<210> 210
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 210

gtggcctcca tatgggccag gac

23

<210> 211

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 211

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcog ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggtacgag 360
gcgagcgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctaccaa ctctctccg acccgctcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccg aggggtcagg 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcgggg gcccgaccgg gaggggctta gggccttccct ggagagggtg 840
gagttcgga gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccg ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgctgca ccgggcagca 1020
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctctc 1140
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gagtggacgg aggacgccc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtctt accacgaggt ggaaaagccc 1320
ctctcccggg tcttgccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380

caggcccttt ccttgagct tgcggaggag atccgccgcc tgcaggagga ggtcttccgc 1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
gagcttaggc ttcccgctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgctg agaagatcct ccagcaccgg 1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgtg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tcccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
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gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctcctgg agggcccccag agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 212

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 212

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 213
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 213
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcgttcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 gggtagaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctggggg ttaccgcgc tcgaggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420
 atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
 cagtgggtgg acttccgcgc cctcgtgggg gacctctccg acaacctccc cggggtcaag 600
 ggcatcgggg agtataccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
 gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
 gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg 840
 gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
 gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc 960

atgtgggcg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgccg ctacgggggg 1200
gagtggacgg aggacgccg ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500
gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgctg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680
acgggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc 1980
ctgatgcgcc gggcgccaa gacggtgaac ttcggcgctc tctacggcat gtccgcccat 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220
gtgaagagcg tcaggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcagtc tcctccaggt cgccaacgag ctctcctcgg agggccccc aagcggggcc 2400
gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 214
<211> 842
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 214

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Tyr Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val

004400 406400 004400

325										330					335				
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val				
		340						345					350						
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly				
		355					360					365							
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu				
	370					375					380								
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly				
	385				390					395				400					
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu				
			405					410						415					
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp				
		420					425					430							
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met				
	435						440					445							
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser				
	450					455					460								
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg				
	465				470					475				480					
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg				
			485					490					495						
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys				
		500						505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535				540									
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
	545				550					555				560					
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
			565					570						575					
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
		580						585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
	610					615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
	625				630				635					640					
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
			645						650					655					

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 215
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 215
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg cgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgaggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcgaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480

gccccgatgc tcctccaggt cgccaacgag ctctctctgg aggcccccca agcgcggggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 216
<211> 842
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 216
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Arg Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 217

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 217

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cggggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgcc ggcgacgacc ccattgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgctggagc tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca cccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccttgg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcacccg cttgggcaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920

Abstract

<211> 839

<212> PRT

<220>

<400> 218

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
		180						185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
	225				230					235					240	
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
			260					265						270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
	275						280					285				
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	
	290					295					300					
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	
	305				310					315					320	
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	
				325					330					335		
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	
			340					345					350			
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
	370					375					380					
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
	385				390					395					400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
			405						410					415		
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420					425					430			
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
	435						440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
	465				470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485					490						495		
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	
			500					505					510			

Arg Ser Ser Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His
835

<210> 219
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 219
cgggacctcg aggcgcgtga accccaggag gtccac 36

<210> 220
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 220
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cgagacggag gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgctc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcggg aaggggctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgtcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
 gtccctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380
 tccctggagg tggccgagga gatcgcccg ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacggggcgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgtcggccca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagacc ctttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 221
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 221
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr		
385					390					395					400		
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn		
				405					410					415			
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg		
			420					425					430				
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr		
			435				440					445					
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val		
	450					455					460						
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly		
465					470					475					480		
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe		
			485						490					495			
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys		
			500					505					510				
Arg	Ser	Ser	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro		
			515				520					525					
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser		
	530					535					540						
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg		
545					550					555					560		
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser		
				565					570					575			
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly		
			580					585					590				
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val		
		595					600					605					
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser		
	610					615					620						
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His		
625					630					635				640			
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp		
				645					650					655			
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr		
			660					665					670				
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu		
		675					680					685					
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val		
	690					695					700						
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr		
705					710					715					720		

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His
835

<210> 222
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 222
ccggggaag tcctcctccg tctcggcccg gccgcctt 39

<210> 223
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 223
gtcggactcg tcaccggtca gggc 24

<210> 224
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (28)..(60)
<223> The bases in these positions within this primer
are 91% of the base shown and 3% each of the other
3 nucleotides.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 224

ctgaccggtg acgagtcga caaccttccc ggggtcaagg gcatcgggga gaggacggcg 60

aggaagcttc tggag

75

<210> 225

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 225

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggcccggc ccccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480

gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caatggcatc 600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgctc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900

cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggac 960

gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020

aaagccctca gggacctgaa ggaggcgagg gggcttctcg ccaaagacct gagcgcttctg 1080

gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccattgctcct cgcctacctc 1140

ctggaccctt cgaacaccac ccccaggggg gtggcccggc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260

cttgaggggg aggagaggct cttttggctt taccgggagg tggagaggcc cttttccgct 1320

gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380

tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560
 gagggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggacc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 226

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 226

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His His
835

<210> 227

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 227

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcttacggg 240
gggtacaagg cgggcccggg ccccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cgcagaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggagggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg cttcttgaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020

aaagccctca gggacctgaa ggagggcgcg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccttttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgcgctcctg 1560
gaggccctcc gcgaggccca ccccatcgct gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgacccttgg ccggacctca tccaccccag gacgggcccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggcttctatc 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
ctccttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400
gcccggtggt ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 228

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 228

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Gln Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Ser Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 229

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 229

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cggcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcattcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatg 600
 ggggagaaga cggggaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

<210> 230
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 230

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130						135				140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Met	Gly	Glu	Lys	Thr	Gly	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His His
 835

<210> 231
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 231
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc ccccaagccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctect ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacccctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaata cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcg accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctccccccc ggcgacgacc ccatgctcct cgctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaagg tctctttga cgagctcagg 1500
cttccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560
gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacgggcccgc 1680
ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggcccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gccacctct ccggcgacga gaacctgate cgggtcttcc aggaggggag ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgtcggccca ccgcctctcc 2040
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
ttccccaagg tgccggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160

gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctccttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 232
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 232
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Asn Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu His His His His His
 835

<210> 233
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 233

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccgggc cccacgccc gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaagc cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ccttctggaa agcccgaagg ccctggagga ggccccctgg 900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc cttttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380
tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500
cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560
gaggccctcc gcgaggcca cccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacggggcgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740

aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
 gccacctct cgggcgacga gaacctgac cgggtcttcc aggaggggag ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tgcgaacga gctggctctc gaggcccaa aagagagggc ggaggccctg 2400
 gcccgctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 234

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 234

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu His His His His His
835

<210> 235
<211> 2517
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 235
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgccc gaggaacttt cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtgttggc 840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accggggccc cgagccttat 1020
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080
gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380

<210> 239
 <211> 839
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 239

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250				255		
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 240
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 240
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag 360
gcggaacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgca cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac 480
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcggcc aggggcgggg gcccgaccgg gaggggctta gggccttctt ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctctccg ccccgagccc 960
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtcca cggggcccc 1020
gagccttata aagccctcag ggacctgaag gaggcgcggg ggcttctcgc caaagacctg 1080
agcgttcttg ccctgaggga aggccttggc ctcccccccg gcgacgacct catgctctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcccggcg ctacggcggg 1200
gagtggacgg aggaggcggg ggagcgggcc gccctttccg agaggctctt cgccaacctg 1260
cttaagaggc ttgaggggga ggagaggctc ctttggcttt accgggagggt ggagaggccc 1320
ctttccgctg tcttgggcca tatggaggcc acgggggtgc gcttgagctt ggcctatctc 1380
agggccttgt ccctggagggt ggccgaggag atcgcccgcc tcgaggccga ggtcttccgc 1440
ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt cctctttgac 1500
gagctagggc ttcccgccat caagaagacg caaaagaccg gcaagcgctc caccagcgcc 1560
gccgtcctgg agggcctccg cgaggccac cccatcgtgg agaagatcct gcagtaccgg 1620
gagctcacca agctgaagag cacctacatt gaccccttgc cggacctcat ccaccccagg 1680
acggggccgc tccacaccg cttcaaccag acggccacgg ccacgggcag gctaagtagc 1740
tccgatccca acctccagaa catccccgtc cgcaccccg c ttgggcagag gatccgcccg 1800
gccttcatcg ccgaggagg gtggctattg gtggccctgg actatagcca gatagagctc 1860
aggggtgctg cccacctctc cggcgacgag aacctgatcc gggctcttcca ggaggggagg 1920
gacatccaca cggagaccgc cagctggatg ttcggcgctc cccgggaggc cgtggacccc 1980
ctgatgcgcc gggcgggcaa gaccatcaac ttcgggggtc tctacggcat gtcggccac 2040
cgctctccc aggagctagc catcccttac gaggaggccc aggccttcat tgagcgctac 2100
tttcagagct tccccagggt gcgggcctgg attgagaaga ccctggagga gggcaggagg 2160

cgggggtacg tggagaccct cttcgggcgc cgccgctacg tgccagacct agaggcccg 2220
 gtgaagagcg tgcgggagggc ggccgagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct ggctatggtg aagctcttcc ccaggctgga ggaaatgggg 2340
 gccaggatgc tccttcaggt cgccaacgag ctggctctcg aggcccaaaa agagagggcg 2400
 gagggcgtgg cccggctggc caaggaggtc atggaggggg tgtatcccct ggccgtgccc 2460
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520
 caccac 2526

<210> 241
 <211> 842
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 241
 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp
 595 600 605
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg
 625 630 635 640
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala
 785 790 795 800
 Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Glu His His His His His His
 835 840

<210> 242
 <211> 2508
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 242

atggaattca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120
ccggtgcaga tgggtctacgg cttcgccccg agcctcctca aggccttgaa ggaggacgga 180
caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240
gcctacaagg cgggcccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac 360
gacgtcctgg gcaccctggc caagaaggcc gaaagggagg ggatggaggt gcgcctcctc 420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480
gggaccctgg tcaccccaaa ggacgtccag gagaagtacg gggtgcccc ggagcgctgg 540
gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccggggt ggcggggata 600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag 660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac 720
ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt 780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg 840
gagttcggaa gcctcctcca cgagttcggc ctctctggag gggagaagcc ccgggaggag 900
gccccctggc ccccgccga aggggccttc gtgggcttcc tcctttcccg caaggagccc 960
atgtgggcgg agcttctggc cctggcggcg gcctcgagg gccgggtcca ccgggcaaca 1020
agcccggttg aggcctggc cgacctcaag gagggccggg ggttcctggc caaggacctg 1080
gccgttttgg ccctgcggga ggggggtggc ctggacccca cggacgacct cctcctggtg 1140
gcctacctcc tggaccggc caacaccac cccgaggggg tggccggcg ctacgggggc 1200
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc 1260
tttaaacggc tttccgagaa gtcctctgg ctctaccagg aggtggagcg gccctctcc 1320
cgggtcttgg ccacatgga gggccggggg gtgaggctgg acgtccccct tctggaggcc 1380
ctctcctttg agctggagaa ggagatggag cgctggagg gggaggctct ccgtttggcc 1440
ggccaccct tcaacctcaa ctcccgcgac cagctggaaa gggctcctct tgacgagctg 1500
ggcctacccc cgggtggggc gacgcagaag acgggcaagc gctccaccgc ccagggggcc 1560
ctggaggccc tccggggggc ccacccatc gtggagctca tcctccagta ccgggagctt 1620
tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccacc gcggacgggc 1680
cggctccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac 1740

cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcattccg caaggccttc 1800
 gtggccgagg aggggtggct ccttttggcg gcggactact cccagattga gctccgggtc 1860
 ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc 1920
 cataccgaga ccgccgcctg gatgttcggc ttagaccccc ctctgggtgga tccaaagatg 1980
 cgccggggcgg ccaagacggt caacttcggc gtctcttacg ggatgtccgc ccacaggctc 2040
 tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag 2100
 agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc 2160
 tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc ccgggtccgc 2220
 tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggccac 2340
 ctctctctcc aagtgcacaa cgagctggtc ctggaggtgc ccgaggaccg ggccgaggag 2400
 gccaaaggccc tggtaagga ggtcatggag aacgcctacc ccctggacgt gccctcgag 2460
 gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggattga 2508

<210> 243
 <211> 835
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 243
 Met Glu Phe Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
 20 25 30
 Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
 35 40 45
 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655
 Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
 770 775 780
 Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu
 785 790 795 800
 Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala
820 825 830

Lys Gln Asp
835

<210> 244
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 244
cttccagaac ctctttaaac ggctttccga gaag 34

<210> 245
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 245
cttctcggaa agccgtttaa agaggttctg gaag 34

<210> 246
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 246
ccggtgggcc ggacgcagaa gacgggcaag c 31

<210> 247
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 247
gcttgcccg tttctgcgtc cggcccaccg g 31

<210> 248
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 248
ctcctccaag tgcacaacga gctggtcctg g

31

<210> 249
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 249
ccaggaccag ctcgttgtgc acttgaggga g

31

<210> 250
<211> 2499
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 250
atggaattcc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc 120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180
gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagacctt cgaggcctac 240
aaggcggggc gggctcccac ccccaggagc tttccccggc agcttgccct tatcaaggag 300
atggtggacc ttttgggcct ggagcgcctc gaggtgcccgg gctttgaagc ggatgacgtc 360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg 420
gaccgggacc ttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac 480
ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540
taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag 600
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg 660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag 720
ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg 780
cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcggaagc 840
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cgagggaagc tccctggccg 900
cccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag 960
cttaacgcct tggccgccgc ctgggagggga agggtttacc gggcgaggga tcccttgagg 1020
gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc 1080
ctgagggaa gatttgccct ggcaccgggc gacgaccca tgctcctcgc ctacctcctg 1140

gatccttcca acaccgcccc cgaaggggta gcccggcgct acggggggga gtggaccgag 1200
gaggcggggg aaagggcgct gctttccgaa aggctttacg ccgccctcct gaagcggtt 1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc 1320
ctggcccaca tggaggccac ggggggtacg ttggatgtgg cctacttaaa ggccctttcc 1380
ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat 1440
cctttcaacc tgaactcccg ggaccagctg gaaagggta tctttgacga gcttgggctt 1500
cccgccatcg gcaagacgca gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560
gccttgcggg aggtcatcc catcgtggac cgcctccttc agtaccggga gctttccaag 1620
ctcaagggaa cctacatcga tcccttgctt gccctggtcc accccaagac gaaccgcctc 1680
cacaccgtt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatcctaata 1740
ctgcaaaata tccccgtgcg caccctttg ggccagcgga tccgcccggc cttcgtggcc 1800
gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg 1860
cacctttccg gggacgagaa cctaattccg gtcttccagg agggccagga catccacacc 1920
cagacggcca gctggatgtt cggcggtgcc ccagaggccg tggattccct gatgcgccgg 1980
gcggccaaaga ccatcaactt cggcgctcctc tacggcatgt ccgcccaccg gctttcgga 2040
gagctggcca tcccctacga ggaggcggtg gccttcatcg agcggtatct ccagagctac 2100
cccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg 2160
gaaaccctct ttggccgccc gcgctacgtg cccgacttgg cttcccgggt gaagagcatc 2220
cgggaggcag cggagcgcat ggccttcaac atgccggtcc aggggaccgc cgcggatttg 2280
atgaaactgg ccatggtgaa gctctttccc aggcttcagg agctgggggc caggatgctt 2340
ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400
caggaggcca agcggaccat ggaggaggtg tggcccctga aggtgccctt ggaggtggaa 2460
gtgggcatcg gggaggactg gctttccgcc aaggcctag 2499

<210> 251

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 251

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	

Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
		20						25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70				75						80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys
	210					215					220				
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys
225					230					235					240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val
			245						250					255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe
			260					265					270		
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
		275					280					285			
Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
	290					295					300				
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu
305					310					315					320
Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala	Glu
				325					330					335	
Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu	Leu
			340					345					350		
Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	Ala
		355					360					365			

Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	
	370					375					380					
Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	
385					390					395					400	
Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	Leu	
				405					410					415		
Leu	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	
			420					425					430			
Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	
		435					440					445				
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	Glu	
	450					455					460					
Ala	Glu	Ile	Arg	Arg	Phe	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	His	
465					470					475					480	
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Ile	Phe	Asp	
				485					490					495		
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys	Arg	
			500					505					510			
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	
		515					520					525				
Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	Thr	
	530					535					540					
Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	Leu	
545					550					555					560	
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	
				565				570						575		
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	
			580					585					590			
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	Val	
		595					600					605				
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	
	610					615					620					
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	Thr	
625					630					635				640		
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Ser	
				645					650					655		
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	
			660					665					670			
Met	Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	
		675					680					685				
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	
	690					695					700					

Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg
725 730 735

Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala
785 790 795 800

Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala
820 825 830

<210> 252

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 252

gccgccctcc tgaagcggct taaggg

26

<210> 253

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 253

cccttaagcc gcttcaggag ggcggc

26

<210> 254

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 254

atcggcaaga cgcagaagac gggcaagc

28

<210> 255
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 255
gcttgcccgt cttctgcgtc ttgccgat 28

<210> 256
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 256
ttgcagggtgc acaacgaact ggtcctc 27

<210> 257
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 257
gaggaccagt tcgttgtgca cctgcaa 27

<210> 258
<211> 2526
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 258
atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120
ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga 180
caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcttacgag 240
gcctacaagg cgggcccggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300
aagcggctgg tggaccttct gggcctgggtc cgcctcgagg ccccggggta cgaggcggac 360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcacctc 420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 260

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 260

atgaattccc tgccctcttt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60

cagaccgcaa gctggatggt cggcggtcccc ccggaggccg tggacccctt gatgcgccgg 1980
gcggccaaga cgggtgaactt cggcggtcctc tacggcatgt ccgcccatag gctctcccag 2040
gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc 2100
cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg 2160
gaaacctctt tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220
agggaggccg cggagcgcat ggccttcaac atgcccgctc agggcaccgc cgcgcacctc 2280
atgaagctcg ccatggtgaa gctcttcccc cgcctccggg agatgggggc ccgcatgctc 2340
ctccaggtcg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg 2400
gctttggcca aggaggccat ggagaaggcc tatccccctg ccgtgcccct ggaggtggag 2460
gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac 2514

<210> 261

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 261

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35				40					45				
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
		130				135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
145				150						155					160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
325 330 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830
 His His His His His His
 835

<210> 262
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 262
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 ccggtgcaga tgggtctacg cttcgcccgg agcctcctca aggccttgaa ggaggacgga 180
 caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240
 gcctacaagg cgggcccggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300
 aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac 360
 gacgtcctgg gcacctggc caagaaggcc gaaaggagg ggatggagg ggcgcatcctc 420
 acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480
 gggaccctgg tcaccccaaa ggacgtccag gagaagtacg gggtgcccc ggagcgctgg 540
 gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccgggtt ggcggggata 600
 ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag 660
 aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac 720
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 aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg 840
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 agcgttcttg ccctgaggga aggccttggc ctcccgccc gcgacgacct catgctcctc 1140
 gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcccggcg ctacggcggg 1200
 gaggtagcgg aggaggcggg ggagcggg ccctttccg agaggctctt cgccaacctg 1260
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 agggccttgt ccctggagggt ggccgaggag atcgcccgc tcgaggccga ggtcttccgc 1440
 ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaagggt cctctttgac 1500
 gagctagggc ttcccgcct caagaagacg caaaagaccg gcaagcgctc caccagcgcc 1560

gccgtcctgg aggccctccg cgaggccac cccatcgtgg agaagatcct gcagtaccgg 1620
 gagctcacca agctgaagag cacctacatt gaccccttgc cggacctcat ccaccccagg 1680
 acgggccgccc tccacacccg cttcaaccag acggccacgg ccacgggcag gctaagtagc 1740
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 gccgccgacc tcatgaagct ggctatggtg aagctcttcc ccaggctgga ggaaatgggg 2340
 gccaggatgc tccttcaggt cgccaacgag ctggtcctcg agggcccaaa agagagggcg 2400
 gaggccgtgg cccggctggc caaggaggtc atggaggggg tgtatcccct ggccgtgccc 2460
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520
 caccac 2526

<210> 263

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 263

Met	Asn	Ser	Thr	Pro	Leu	Phe	Asp	Leu	Glu	Glu	Pro	Pro	Lys	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		
Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Arg	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Gln	Ala	Val	Val
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
	65				70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	

Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser
 450 455 460
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp
 595 600 605
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg
 625 630 635 640
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala
785 790 795 800

Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Glu His His His His His
835 840

<210> 264

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 264

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180
gtgatcgtgg tgtttgacgc caaggcccc tccttcgcgc accagacctt cgaggcctac 240
aaggcggggc gggctccacc ccccaggac tttcccgcgc agcttgcctt tatcaaggag 300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc 360
ctggctaccc tggccaagaa ggcggaagaa gaaggctacg aagtgcgcac cctcaccgcg 420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac 480
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aagacggcgc ccaagctgat ccgggagtg ggaagcctgg aaaaccttct taagcacctg 660
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cggctggcca aggaggtcat ggaggggggtg tatcccctgg ccgtgcccct ggaggtggag 2460
gtggggatag gggaggactg gctctccgcc aaggagcacc accaccacca ccac 2514

<210> 265

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 265

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700

ggcagcctcc	tccacgagtt	cggcctcctg	gaggcccccg	ccccctgga	ggaggcccc	900
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gcggagctta	aagccctggc	cgcttgcagg	gacggccggg	tgcaccgggc	agcagacccc	1020
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ctcgcccacc	tctccgggga	cgaaaacctg	atcagggtct	tccaggaggg	gaaggacatc	1920
cacaccaga	ccgcaagctg	gatgttcggc	gtccccccgg	aggccgtgga	ccccctgatg	1980
cgccgggcgg	ccaagacggt	gaacttcggc	gtcctctacg	gcatgtccgc	ccataggctc	2040
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agcttcccca	aggtgcgggc	ctggatagaa	aagacctggg	aggaggggag	gaagcggggc	2160
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atgctcctcc	aggtccacga	cgagctcctc	ctggaggccc	cccaagcgcg	ggccgaggag	2400
gtggcggtct	tggccaagga	ggccatggag	aaggcctatc	ccctcgccgt	gccctggag	2460
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<210> 267
<211> 834
<212> PRT
<213> Thermus aquaticus
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<400> 267

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130 135 140
Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145 150 155 160
Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195 200 205
Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210 215 220
Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225 230 235 240
Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
245 250 255
Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260 265 270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275 280 285
Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
290 295 300
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305 310 315 320
Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg

325																330				335			
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly								
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp								
Leu	Val 370	Pro	Gly	Asp	Asp	Pro 375	Met	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro								
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400								
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg								
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly	Glu 425	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr								
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala								
Thr	Gly 450	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu								
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480								
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu								
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly								
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His								
Pro	Ile 530	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys								
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560								
Arg	Leu	His	Thr	Arg 565	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu								
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu								
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu								
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu								
Ser 625	Gly	Asp	Glu	Asn 630	Leu	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640								
His	Thr	Gln	Thr	Ala 645	Ser	Trp	Met	Phe	Gly 650	Val	Pro	Pro	Glu	Ala 655	Val								

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly

<210> 268
 <211> 832
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 268
 Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
 1 5 10 15
 Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
 20 25 30
 Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala

Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu
 450 455 460
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg
 725 730 735
 Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala
785 790 795 800

Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala
820 825 830

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

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cgc 63

<210> 270
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

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<210> 271
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

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<220>
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<220>
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<212> DNA
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36

*Sub
B
Concluded*

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